

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Gentz, Reiner  
Fleischmann, Robert D.
- (ii) TITLE OF INVENTION: 5-LIPOXYGENASE-ACTIVATING PROTEIN II
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: JAMES H. DAVIS  
HUMAN GENOME SCIENCES, INC.
  - (B) STREET: 9410 KEY WEST AVENUE
  - (C) CITY: ROCKVILLE
  - (D) STATE: MD
  - (E) COUNTRY: USA
  - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: DIVISIONAL OF US 08/264,003
  - (B) FILING DATE: HERewith
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: JONATHAN L. KLEIN
  - (B) REGISTRATION NUMBER: 41,119
  - (C) REFERENCE/DOCKET NUMBER: PF122P1D1
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 301-309-8504
  - (B) TELEFAX: 301-309-8439

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 444 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..441
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCC GGG AAC TCG ATC CTG CTG GCT GCT GTC TCT ATT CTC TCG GCC

Met	Ala	Gly	Asn	Ser	Ile	Leu	Leu	Ala	Ala	Val	Ser	Ile	Leu	Ser	Ala		
1				5					10						15		
TGT	CAG	CAA	AGT	TAT	TTT	GCT	TTG	CAA	GTT	GGA	AAG	GCA	AGA	TTA	AAA		96
Cys	Gln	Gln	Ser	Tyr	Phe	Ala	Leu	Gln	Val	Gly	Lys	Ala	Arg	Leu	Lys		
			20					25					30				
TAC	AAA	GTT	ACG	CCC	CCA	GCA	GTC	ACT	GGG	TCA	CCA	GAG	TTT	GAG	AGA		144
Tyr	Lys	Val	Thr	Pro	Pro	Ala	Val	Thr	Gly	Ser	Pro	Glu	Phe	Glu	Arg		
		35					40					45					
GTA	TTT	CGG	GCA	CAA	CAA	AAC	TGT	GTG	GAG	TTT	TAT	CCT	ATA	TTC	ATA		192
Val	Phe	Arg	Ala	Gln	Gln	Asn	Cys	Val	Glu	Phe	Tyr	Pro	Ile	Phe	Ile		
	50					55				60							
ATT	ACA	TTG	TGG	ATG	GCT	GGG	TGG	TAT	TTC	AAC	CAA	GTT	TTT	GCT	ACT		240
Ile	Thr	Leu	Trp	Met	Ala	Gly	Trp	Tyr	Phe	Asn	Gln	Val	Phe	Ala	Thr		
	65				70				75					80			
TGT	CTG	GGT	CTG	GTG	TAC	ATA	TAT	GGC	CGT	CAC	CTA	TAC	TTC	TGG	GGA		288
Cys	Leu	Gly	Leu	Val	Tyr	Ile	Tyr	Gly	Arg	His	Leu	Tyr	Phe	Trp	Gly		
			85					90					95				
TAT	TCA	GAA	GCT	GCT	AAA	AAA	CGG	ATC	ACC	GGT	TTC	CGA	CTG	AGT	CTG		336
Tyr	Ser	Glu	Ala	Ala	Lys	Lys	Arg	Ile	Thr	Gly	Phe	Arg	Leu	Ser	Leu		
			100				105					110					
GGG	ATT	TTG	GCC	TTG	TTG	ACC	CTC	CTA	GGT	GCC	CTG	GGA	ATT	GCA	AAC		384
Gly	Ile	Leu	Ala	Leu	Leu	Thr	Leu	Leu	Gly	Ala	Leu	Gly	Ile	Ala	Asn		
		115				120					125						
AGC	TTT	CTG	GAT	GAA	TAT	CTG	GAC	CTC	AAT	ATT	GCC	AAG	AAA	CTG	AGG		432
Ser	Phe	Leu	Asp	Glu	Tyr	Leu	Asp	Leu	Asn	Ile	Ala	Lys	Lys	Leu	Arg		
	130					135				140							
CGG	CAA	TTC	TAA														444
Arg	Gln	Phe															
145																	

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Gly	Asn	Ser	Ile	Leu	Leu	Ala	Ala	Val	Ser	Ile	Leu	Ser	Ala		
1				5					10						15		
Cys	Gln	Gln	Ser	Tyr	Phe	Ala	Leu	Gln	Val	Gly	Lys	Ala	Arg	Leu	Lys		
			20					25					30				
Tyr	Lys	Val	Thr	Pro	Pro	Ala	Val	Thr	Gly	Ser	Pro	Glu	Phe	Glu	Arg		
		35					40					45					
Val	Phe	Arg	Ala	Gln	Gln	Asn	Cys	Val	Glu	Phe	Tyr	Pro	Ile	Phe	Ile		

50                      55                      60  
 Ile Thr Leu Trp Met Ala Gly Trp Tyr Phe Asn Gln Val Phe Ala Thr  
 65                      70                      75                      80  
 Cys Leu Gly Leu Val Tyr Ile Tyr Gly Arg His Leu Tyr Phe Trp Gly  
                     85                      90                      95  
 Tyr Ser Glu Ala Ala Lys Lys Arg Ile Thr Gly Phe Arg Leu Ser Leu  
                     100                      105                      110  
 Gly Ile Leu Ala Leu Leu Thr Leu Leu Gly Ala Leu Gly Ile Ala Asn  
                     115                      120                      125  
 Ser Phe Leu Asp Glu Tyr Leu Asp Leu Asn Ile Ala Lys Lys Leu Arg  
                     130                      135                      140  
 Arg Gln Phe  
 145

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGGGATCC GCCGGGAACG CGATCCTGCT GGCTGCT

37

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGCAAGCTT AGAATTGCCG CCTCAGTTTC TTGGC

35

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGATCCGC CACCATGGCC GGGAACTCGA TCCT

34

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACAGGTACC AGCTTCTGCA AGCATTAAAG

30

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 160 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asp Gln Glu Thr Val Gly Asn Val Val Leu Leu Ala Ile Val Thr  
1                      5                      10                      15

Leu Ile Ser Val Val Gln Asn Gly Phe Phe Ala His Lys Val Glu His  
20                      25                      30

Glu Ser Arg Thr Gln Asn Gly Arg Ser Phe Gln Arg Thr Gly Thr Leu  
35                      40                      45

Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp Ala Tyr  
50                      55                      60

Pro Thr Phe Leu Ala Val Leu Trp Ser Ala Gly Leu Leu Cys Ser Gln  
65                      70                      75                      80

Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg Gln Lys  
85                      90                      95

Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro Gly Tyr  
100 105 110

Ile Phe Gly Lys Arg Ile Ile Leu Phe Leu Phe Leu Met Ser Val Ala  
115 120 125

Gly Ile Phe Asn Tyr Tyr Leu Ile Phe Phe Gly Ser Asp Phe Glu Asn  
130 135 140

Tyr Ile Lys Thr Ile Ser Thr Thr Ile Ser Pro Leu Leu Leu Ile Pro  
145 150 155 160